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RAW SEQUENCE LISTING

DATE: 10/16/2001 TIME: 15:02:12

PATENT APPLICATION: US/09/923,444

Input Set : N:\Crf3\RULE60\09923444.txt Output Set: N:\CRF3\10162001\I923444.raw

SEQUENCE LISTING

			PEQUENCE DISTING	
	4 (1) GENERAL I	NFORMATION:	
	6	(i) APPL	ICANT: LI, YI	
	7		FLEISCHMANN, ROBERT	
	9	(ii) TITL	E OF INVENTION: NEUROTRANSMITTER TRANSPORTER	
	11	(iii) NUMB	DER OF SEQUENCES: 6	
	13	(iv) CORR	ESPONDENCE ADDRESS:	
	14	(A)	ADDRESSEE: Human Genome Sciences, Inc.	
	15	(B)	ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville	
	16		CITY: Rockville	
	17	(D)	STATE: ND	
	18	(E)	COUNTRY: US	
	19	(F)	ZIP: 20850	
	21	(V) COMP	PUTER READABLE FORM:	
	22	(A)	MEDIUM TYPE: Floppy disk	
	23	(B)	COMPUTER: IBM PC compatible	
	24	(C)	OPERATING SYSTEM: PC-DOS/MS-DOS	
	25	(D)) SOFTWARE: PatentIn Release #1.0, Version #1.30	
	27	(vi) CURF	RENT APPLICATION DATA:	
C>	28	· (A)) APPLICATION NUMBER: US/09/923,444	
C>	29	(B)) FILING DATE: 08-Aug-2001	
	30	(C)) CLASSIFICATION:	
	32	(vii) PRIC	OR APPLICATION DATA:	
	33	(A)) APPLICATION NUMBER: 09/062,815	
	34	(B)) FILING DATE: 199-12-20	
	36	(viii) ATT	ORNEY/AGENT INFORMATION:	
	37	(A) NAME: Michele M. Wales) REGISTRATION NUMBER: 43,975	
	38	(В) REFERENCE/DOCKET NUMBER: PF116	
	39	(C	ECOMMUNICATION INFORMATION:	
	41	(1X) TEL) TELEPHONE: (301) 309-8504	
	42	A)) TELEFAX: (301) 309-8439	
	43	(D	ION FOR SEQ ID NO: 1:	
	46	(Z) INFORMAT	UENCE CHARACTERISTICS:	
	48	(T) 2EA) LENGTH: 2485 base pairs	
	49	(A	3) TYPE: nucleic acid	
	50 51	(C	STRANDEDNESS: single	
	51 52	(0	O) TOPOLOGY: linear	
	54	/ii) MOT	LECULE TYPE: DNA (genomic)	
	57	(ix) FEA		
	58		A) NAME/KEY: CDS	
	59	(B	3) LOCATION: 2662446	
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			TO CONTROL OF A CONTROL OF THE CONTR	120
			TOTAL COLOR CONTROL ACCIDED TO THE COLOR COLORS	180
			AGGGGGGACA CHI CCACCCCCCC AGTCTGCGCG ACTACCCACG CGTGTGTGC	240
	70	CCCTGAATGA G	GAAGGAGT GCACGGGCC MOTOTOCATCT TCTCTGTGTG CTGGGGAGCA	240

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72 GGGCTACACG GCCCAGGTGG CATCA ATG CCG AAG AAC AGC AAA GTG ACC CAG 73 Met Pro Lys Asn Ser Lys Val Thr Gln 1 5	292
74 76 CGT GAG CAC AGC AGT GAG CAT GTC ACT GAG TCC GTG GCC GAC CTG CTG	340
76 CGT GAG CAC AGC AGT GAG CAI GTO HOT GIU SER Val Ala Asp Leu Leu 77 Arg Glu His Ser Ser Glu His Val Thr Glu Ser Val Ala Asp Leu Leu 25	
70 10 15 20 23	
20 CTC CAG CAG CCT GTG GAC TAT AAG CAG AGT GTA CTG AAT GTG GCT	388
81 Ala Leu Glu Glu Pro Val Asp Tyr Lys Gln Ser Val Leu Asn Val Ala	
30 35	
AA CCT CAC CCA CCC CCC AAG CAG AAG GCG GTG GAG GAG GAG CTG GAT GCA	436
85 Gly Glu Ala Gly Gly Lys Gln Lys Ala Val Glu Glu Glu Leu Asp Ala	
06 45 50	404
AN CAC CAC CCC CCC CCC TGG AAC AGT AAG CTG CAG TAC ATC CTG GCC CAG	484
89 Glu Asp Arg Pro Ala Trp Asn Ser Lys Leu Gin Tyr 11e Leu Ala Gin	
00 60 65 70	532
92 ATT GGC TTC TCT GTG GGC CTC GGC AAC ATC TGG AGG TTC CCC TAC CTG	332
93 The Gly Phe Ser Val Gly Leu Gly Ash The Trp Arg Phe Pro Tyl Leu	
04 75 80	580
96 TGC CAG AAA AAT GGA GGA GGT GCT TAC CTG GTG CCC TAC CTG GTG CTG	300
97 Cys Gln Lys Asn Gly Gly Gly Ala Tyr Leu Val Pro Tyr Leu Val Leu 105	
00:00	628
100 CTG ATC ATC GGG ATC CCC CTC TTC TTC CTG GAG CTG GCT GTG GGT	
100 CTG ATC ATC GOS MIC SOS LEU Phe Phe Leu Glu Leu Ala Val Gly 101 Leu Ile Ile Gly Ile Pro Leu Phe Phe Leu Glu Leu Ala Val Gly 115	
100 110 =	676
102 104 CAG AGG ATC CGC CGC GGA AGC ATC GGT GTG TGG CAC TAT ATA TGT CCC 104 CAG AGG ATC CGC CGC GGA AGC ATC GGT GTG TGG CAC TAT ATA TGT CCC	
104 CAG AGG ATC COSC COSC COM HOS HIS THE GLY Val Trp His Tyr Ile Cys Pro 105 Gln Arg Ile Arg Arg Gly Ser Ile Gly Val Trp His Tyr Ile Cys Pro 106 135	
106 125 130 130 130 130 130 130 130 130 130 130	724
108 CGC CTG GGG GGG ATC GGC ITC ICC AGC IGG MIN OF THE Phe Val 109 Arg Leu Gly Gly Ile Gly Phe Ser Cys Ile Val Cys Leu Phe Val	
145	
110 140 145 145 150 170 170 170 170 170 170 170 170 170 17	772
112 GGG CTG TAT TAT ANY GTG ATC ATC GGG TTP Ser Ile Phe Tyr Phe Phe 113 Gly Leu Tyr Tyr Asn Val Ile Ile Gly Trp Ser Ile Phe Tyr Phe Phe	
114 155 160	
116 ANG THE CAG THE CCG CTG CCC TGG AGT GAA TGT CCT GTC GTC AGG	820
116 AAG ICC IIC CAG IAC COS GIO DIO TYP Ser Glu Cys Pro Val Val Arg 117 Lys Ser Phe Gln Tyr Pro Leu Pro Trp Ser Glu Cys Pro Val Val Arg	
110 170 175 180	2.50
130 AME CCC ACC CTC CCA GTG GTG GAG GCA GAG TGT GAA AAG AGC TCA GCC	868
121 Asn Gly Ser Val Ala Val Val Glu Ala Glu Cys Glu Lys Ser Ser Alu	
100 190	016
134 ACT ACC TAC TTC TGG TAC CGA GAG GCT TTG GAC ATC TCT GAC TCC ATC	916
125 Thr Thr Tyr Phe Trp Tyr Arg Giu Ala Leu Asp lie Sel Asp Sel 110	
100 205 210	064
100 MCC CAG AGT GGG GGC CTC AAC TGG AAG ATG ACC CTG TGC CTC CIC GIG	964
129 Ser Glu Ser Gly Gly Leu Asn Trp Lys Met Thr Leu Cys Leu Leu Vul	-
120 220 225 250	1012
133 CMC MCC ACC ATC GGG GGG ATG GCT GTC GGT AAG GGC ATC CAG TCC TCG	1012
133 Val Trp Ser Ile Gly Gly Met Ala Val Gly Lys Gly Ile Gin Ser Ser	
124 225 240 245	1060
134 233 136 GGG AAG GTG ATG TAT TTC AGC TCC CTC TTC CCC TAC GTG GTG CTG GCC	1000

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137	Glv	Lys	Val	Met	Tyr	Phe	Ser	Ser	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ala	
1 2 0	050					255					200					200	1108
140	maa	TTC	CTG	GTC	CGG	GGG	TTG	TTG	TTG	CGA	GGG	GCA	GTT	GAT	GGC	AIC Tlo	1100
141	Cys	Phe	Leu	Val	Arg	Gly	Leu	Leu	Leu	Arg	Gly	Ala	vai	Asp	280	TTE	
1 4 2					270					2/3					200		1156
144	CTA	CAC	ATG	TTC	ACT	CCC	AAG	CTG	GTC	AAG	ATG	CTG	GAC	Dro	Cln	Val	1130
145	Leu	His	Met	Phe	Thr	Pro	Lys	Leu	Val	Lys	мет	ьeu	ASP	295	GIII	VUI	
				205					290					200			1204
148	TGG	CGG	GAG	GTA	GCT	ACC	CAG	GTC	TTC	TTT	GGC	110	Clv	LAII	Glv	Phe	
149	${\tt Trp}$	Arg	Glu	Val	Ala	Thr	GIn	vai	Phe	Pne	СТА	ьец	310	пец	O ± j	1 110	
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	Gly		Val	ITe	vaı	Pne	320	Ser	Tyr	A3II	LJS	325				-	
154		315	a	222	000	CITIC	320 CTC	m'CC	TTC	ΔΤΟ	AAC		TTC	ACG	TCA	GTG	1300
156	CAC	TTC	GAT	GGC	310	TOU	U = 1	Sar	Phe	Tle	Asn	Phe	Phe	Thr	Ser	Val	
		Phe	Asp	GIY	Ald	335	Val	Ser	1110	110	340	•				345	
158	330	000	3.00	ama	cmc	CTC	արարար	стт	GTT	ттG		TTC	AAG	GCC	AAC	ATC	1348
160	TTG	GCC	ACC	LOU	U a 1	Val	Dhe	Val	Val	Leu	Gly	Phe	Lys	Ala	Asn	Ile	
		Ala	THE	neu	350	Val	1110	, 42		355			-		360		
162	3 m.c	ת א א	CAG	λAC	тст	GTG	GTC	GAG	AAT	GCT	GAG	AAA	ATC	CTA	GGG	TAC	1396
164	Mot	AAI	GAG	T.VS	Cvs	Val	Val	Glu	Asn	Ala	Glu	Lys	Ile	Leu	Gly	Tyr	
100				265					370					3/3			
1.00	ama.	አአር	ልሮሮ	አአሮ	GTC	CTG	AGC	CGG	GAC	CTC	ATC	CCA	CCC	CAC	GTC	AAC Asn	1444
160	Len	Agn	Thr	Asn	Val	Leu	Ser	Arg	Asp	Leu	Ile	Pro	Pro	His	Val	Asn	
170			200					- 385					330				1400
170	mma	TCC	(2) (2)	CTC	ACC	ACA	AAG	GAC	TAC	ATG	GAG	ATG	GAC	AAT	GTC	ATC	1492
173	Phe	Ser	His	Leu	Thr	Thr	Lys	Asp	Tyr	Met	Glu	Met	Asp	Asn	Val	Ile	
174		205					400					400	,				1540
170	3.000	3.00	CITC	AAG	GAG	GAC	CAG	TTC	TCA	GCC	CTG	GGC	CTI	GAC	CCC	TGC	1540
177	Met	Thr	· Val	Lys	Glu	Asp	Gln	Phe	Ser	Ala	. ьег	і Сту	Leu	Asp	Pro	Cys 425	
170	410					415					420	,				125	1588
180	CTI	CTC	GAG	GAC	GAG	CTG	GAC	AAG	TCC	GTG	CAG	GGC	ACE		. CIG	GCC	1300
181	Leu	Let	ı Glu	ı Asp	Glu	Leu	Asp	Lys	Ser	vaı	. GII	ı Gıy	Thi	. Ст	440	niu	
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184	TTC	ATO	GCC	TTC	: ACI	GAG	GCC	ATG	ACG	CAC	TTC	Dec	, ACC	. ICC	. Dro	TTC	
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186	5			445	5				450	) 1 3 m/	* **	т <i>С</i> тС	e aga			AGC	1684
188	3 TGC	TC	C GT	ATO	TTC	TTC	TTC	ATC	CTI	T1	, AA	. T.O.	, G1v	, Lei	Gly	AGC Ser	
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190	)		460	) 			ccc	40. አመረ	י אריר	• ACC	: CC	т атс			ACC	TCC r Ser	1732
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500 E 20	
510 515 520 510 515 575 ATC	1876
202 510 510 510 510 510 510 510 510 510 510	
205 Met Phe Asp Asp Tyr Ser Ald III Led 110 Ded 111	
205 Nec 1110 11-1 1 530 530 530 770 ATC ATC	1924
206 525 208 CTT GAG AAC ATC GCT GTG GCC TGG ATT TAT GGA CCC AAG AAG TTC ATG 208 CTT GAG AAC ATC GCT GTG GCC TGG ATT TAT GGA CCC AAG AAG TTC ATG	
and the Clu App The Ala Val Ala Tip Tie Tit Cir T	
210 540 545 550	1972
210 540 545 212 CAG GAG CTG ACG GAG ATG CTG GGC TTC CGC CCC TAC CGC TTC TAT TTC 212 CAG GAG CTG ACG GAG ATG CTG GGC TTC CGC CCC TAC CGC TTC TAT TTC	
212 Cln Clu Leu Thr Glu Met Leu Gry File Arg 110 -1-	
	2020
214 555 560 216 TAC ATG TGG AAG TTC GTG TCT CCA CTA TGC ATG GCT GTG CTC ACC ACA 216 TAC ATG TGG AAG TTC GTG TCT CCA CTA TGC ATG GCT GTG CTC ACC ACA	
217 Tur Met Tro Lvs Phe Val Ser Plo Deu Cys Mes 112	
218 570 575 580 575 580 575	2068
218 570 220 GCC AGC ATC ATC CAG CTG GGG GTC ACG CCC CCG GCC TAC AGC GCC TGG 220 GCC AGC ATC ATC CAG CTG GGG GTC ACG CCC CCG GCC TAC AGC GCC TGG	
221 Ala Ser Ile Ile Gin Leu Giy vai illi 110 110 110 110 110 110 110 110 110 11	
590 595 TARE THE TOTAL THE	2116
222 590 224 ATC AAG GAG GAG GCT GCC GAG CGC TAC CTG TAT TTC CCC AAC TGG CCC 224 ATC AAG GAG GAG GCT GCC GAG CGC TAC CTG TAT TTC CCC AAC TGG CCC	
225 The Lys Glu Glu Ala Ala Glu Arg Tyr Lea Tyr 120	
226 605 610 CCC ACC CTG CCC ATC CCT	2164
226 605 010 228 ATG GCA CTC CTG ATC ACC CTC ATC GTC GTG GCG ACG CTG CCC ATC CCT 228 ATG GCA CTC CTG ATC ACC CTC ATC Wal val Ala Thr Leu Pro Ile Pro	
229 Met Ala Leu Leu Ile Thr Leu Ile Val Val Ala 200	
	2212
230 620 CAC TTC CAC CTG CTC TCT GAT GGC TCC AAC 232 GTG GTG TTC GTC CTG CGG CAC TTC CAC CTG CTC TCT GAT GGC TCC AAC	
233 Val Val Phe Val Leu Arg His Phe His Leu Beu Beu CAF	
	2260
234 635 640 236 ACC CTC TCC GTG TCC TAC AAG AAG GCC CGC ATG ATG AAG GAC ATC TCC	
236 ACC CTC TCC GTG TCC TAC AAG AAG GCC COO HITC 237 Thr Leu Ser Val Ser Tyr Lys Lys Ala Arg Met Met Lys Asp Ile Ser 660 665	
238 650 CCC ACC CCC TTC ATC CTC AGC AAG GTG CCC	2308
240 AAC CTG GAG GAG AAC GAT GAG ACC CGG 116 Mrs of Ser Lys Val Pro 241 Asn Leu Glu Glu Asn Asp Glu Thr Arg Phe Ile Leu Ser Lys Val Pro 675 680	
241 Asn Leu Glu Glu Asn Asp Glu IIII Arg III 670 680	
242 OCC. AMG. CCC. ACT. CAC. CGT. TCC. TAT. CTG. GGG. CCC.	2356
244 AGT GAG GCA CCT TCC CCC ATG CCC ACT CRO Ser Tyr Leu Gly Pro 245 Ser Glu Ala Pro Ser Pro Met Pro Thr His Arg Ser Tyr Leu Gly Pro 695	
245 Ser Glu Ala Pro Ser Plo Met 115 1112 112 1	
246 CCC AAT GGA CCC TAT	2404
248 GGC AGC ACA TCA CCC CTG GAG ACC AGC TGG TAIL 249 GLy Ser Thr Ser Pro Leu Glu Thr Ser Trp Asn Pro Asn Gly Pro Tyr	
	2446
250 FIG. CHC. CHC. GCC. AGC. ACC. CCT. GAG. TCT. GAG. CTG.	2446
252 GGG CGC GGC TAC CTG CTG GCC Not floor	
	2495
254 715 256 TGACCACTGC CCAAGCCCAT GCCCGCTCTC CCCCCACCG	2485
256 TGACCACIGE CCARACTERIST 10 NO: 2: 259 (2) INFORMATION FOR SEQ ID NO: 2:	
mramit. 707 amino acios	
ino agid	
- monorocy, linear	
MOT FOULE TYPE: protein	
268 (xi) SEQUENCE DESCRIPTION. SEQ 15 Not 2.70 Met Pro Lys Asn Ser Lys Val Thr Gln Arg Glu His Ser Ser Glu His	
2/0 rcc 110 =1	

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271 273 \	1 Val	Thr	Glu	Ser	Val	Ala	Asp	Leu	Le	ı A	la	Leu	Glu	Glu	Pro 30	Val	Asp	Þ
274				20					2!	) - «	17	C111	λla	G1 v	Glv	Lvs	Gli	a
274 276 '	Tyr	Lys	Gln	Ser	Val	Leu	Asn	Val	AL	a G	тА	GIU	Ата	45	011		-	
277 279	LVS	Ala	Val	Glu	Glu	Glu	Leu	Asp	Al	a G	Lu	Asp	Arg	PIO	Alu	115		
280 282	Ser	Lvs	Leu	Gln	Tyr	Ile	Leu	Ala	Gl	n I	lle	GTĀ	Pne	ser	Val	GIY	В	n
202	65	-1-			-	70						75			a1	C1 **	C1	77
283 285	C1v	Δen	Tle	Trp	Arq	Phe	Pro	Tyr	Le	u C	Cys	Gln	Lys	Asn	GIY	GTÄ	GI	Y
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289	T	Dho	Phe	Len	Glu	Leu	Ala	Val	. G1	y (	Gln	Arg	Ile	Arg	Arg	GTĀ	Se	ı
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294	He	GIY	Val	111	пто	+ I +	135	-1			_		140					
295		130	Cys	T10	17 - 1	Cvc	Len	Phe	. Va	1 (	Gly	Leu	Tyr	Tyr	Asn	val	L Il	.e
297	Ser	Ser	Cys	TTE	Val	150	шси			-		155					16	50
298	145		Trp	_	<b>-1</b> -	120	, Пттт	Dhe	a Dł	10	Lvs	Ser	Phe	Gln	Туг	r	) Le	∍u
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315	Ala	va:	l Gly	y Lys	s Gly	y Ile	e Gl	n Se	r S	er	GIA	у гуз	s va.	LINC	C 11	25	5	
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34	3 38	5				3	90											

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]